

SEQUENCE LISTING

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AKASHI, TOMOYOSHI
AOKI, TOSHIO

<120> POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE
DEHYDRATASE AND APPLICATION OF THE SAME

<130> 8062-1031

<140> 10/551,665
<141> 2005-09-28

<150> PCT/JP04/04214
<151> 2004-03-25

<150> JP 2003-092337
<151> 2003-03-28

<160> 10

<170> PatentIn Ver. 3.3

<210> 1
<211> 328
<212> PRT
<213> Glycyrrhiza echinata

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Leu Gly Ser Ser Phe Val Pro Pro Ser Pro Glu Asp Pro Glu Thr Gly
35 40 45
Val Ser Thr Lys Asp Ile Val Ile Ser Glu Asn Pro Thr Ile Ser Ala
50 55 60
Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr Thr Glu Lys Leu Pro Ile
65 70 75 80
Leu Val Tyr Tyr His Gly Gly Ala Phe Cys Leu Glu Ser Ala Phe Ser
85 90 95
Phe Leu His Gln Arg Tyr Leu Asn Ile Val Ala Ser Lys Ala Asn Val
100 105 110
Leu Val Val Ser Ile Glu Tyr Arg Leu Ala Pro Glu His Pro Leu Pro
115 120 125
Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu Lys Trp Val Thr Ser His
130 135 140

Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala Asp Pro Trp Leu Ile Lys
 145 150 155 160

His Gly Asp Phe Asn Arg Phe Tyr Ile Gly Gly Asp Thr Ser Gly Ala
 165 170 175

Asn Ile Ala His Asn Ala Ala Leu Arg Val Gly Ala Glu Ala Leu Pro
 180 185 190

Gly Gly Leu Arg Ile Ala Gly Val Leu Ser Ala Phe Pro Leu Phe Trp
 195 200 205

Gly Ser Lys Pro Val Leu Ser Glu Pro Val Glu Gly His Glu Lys Ser
 210 215 220

Ser Pro Met Gln Val Trp Asn Phe Val Tyr Pro Asp Ala Pro Gly Gly
 225 230 235 240

Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala Pro Gly Ala Pro Asn Leu
 245 250 255

Ala Thr Leu Gly Cys Pro Lys Met Leu Val Phe Val Ala Gly Lys Asp
 260 265 270

Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr Glu Ala Val Lys Glu Ser
 275 280 285

Gly Trp Lys Gly Asp Val Glu Leu Ala Gln Tyr Glu Gly Glu His
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Cys Phe Gln Ile Tyr His Pro Glu Thr Glu Asn Ser Lys Asp Leu Ile
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Gly Arg Ile Ala Ser Phe Leu Val
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<212> DNA

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<220>

<221> CDS

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gga acc gtg gag cga ttc cta ggc tca tcg ttt gta cca cct tcc cct	148
Gly Thr Val Glu Arg Phe Leu Gly Ser Ser Phe Val Pro Pro Ser Pro	
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gaa gac ccc gaa aca ggg gtt tcc acg aaa gac ata gta atc tca gaa Glu Asp Pro Glu Thr Gly Val Ser Thr Lys Asp Ile Val Ile Ser Glu	196
45 50 55	
aac ccc acc atc tct gct cgc gtt tac ctt cca aaa ctg aac aac acc Asn Pro Thr Ile Ser Ala Arg Val Tyr Leu Pro Lys Leu Asn Asn Thr	244
60 65 70	
acc gag aag ctc cca atc ttg gtc tac tac cac ggc ggc gcg ttc tgc Thr Glu Lys Leu Pro Ile Leu Val Tyr Tyr His Gly Gly Ala Phe Cys	292
75 80 85 90	
ctc gaa tct gct ttc tcc ttc ctc cac caa cgc tac ctc aac atc gtt Leu Glu Ser Ala Phe Ser Phe Leu His Gln Arg Tyr Leu Asn Ile Val	340
95 100 105	
gct tcc aag gca aat gtt cta gta gtt tcc atc gag tac agg ctc gcc Ala Ser Lys Ala Asn Val Leu Val Val Ser Ile Glu Tyr Arg Leu Ala	388
110 115 120	
cca gaa cac cct ctt ccg gct gca tat gaa gat ggt tgg tat gct ctc Pro Glu His Pro Leu Pro Ala Ala Tyr Glu Asp Gly Trp Tyr Ala Leu	436
125 130 135	
aaa tgg gtc act tct cat tcc aca aac aac aaa ccc acc aac gct Lys Trp Val Thr Ser His Ser Thr Asn Asn Asn Lys Pro Thr Asn Ala	484
140 145 150	
gac cca tgg ttg atc aaa cac ggt gat ttc aac agg ttc tac atc ggg Asp Pro Trp Leu Ile Lys His Gly Asp Phe Asn Arg Phe Tyr Ile Gly	532
155 160 165 170	
ggt gac act tct ggt gca aac att gca cac aat gcg gct ctt cgt gtt Gly Asp Thr Ser Gly Ala Asn Ile Ala His Asn Ala Ala Leu Arg Val	580
175 180 185	
ggt gct gag gcc tta cct ggg ggg ctg aga ata gca ggg gta ctc tct Gly Ala Glu Ala Leu Pro Gly Gly Leu Arg Ile Ala Gly Val Leu Ser	628
190 195 200	
gct ttt cct ctg ttt tgg ggt tct aag cct gtt ttg tca gaa cct gtc Ala Phe Pro Leu Phe Trp Gly Ser Lys Pro Val Leu Ser Glu Pro Val	676
205 210 215	
gag ggg cat gag aag agc tca ccc atg caa gtt tgg aac ttt gtg tac Glu Gly His Glu Lys Ser Ser Pro Met Gln Val Trp Asn Phe Val Tyr	724
220 225 230	
cca gat gca cca ggt ggc ata gat aac cca cta atc aac cct ttg gca Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Leu Ile Asn Pro Leu Ala	772
235 240 245 250	
cct ggg gct cct aac ttg gcc aca ctt ggg tgt cca aag atg ttg gtc Pro Gly Ala Pro Asn Leu Ala Thr Leu Gly Cys Pro Lys Met Leu Val	820
255 260 265	

ttt gtt gcg ggg aag gat gat ctt aga gac aga ggg att tgg tac tat	868
Phe Val Ala Gly Lys Asp Asp Leu Arg Asp Arg Gly Ile Trp Tyr Tyr	
270 275 280	
gag gct gtg aag gaa agt ggg tgg aaa ggg gat gtg gaa ctt gct cag	916
Glu Ala Val Lys Glu Ser Gly Trp Lys Gly Asp Val Glu Leu Ala Gln	
285 290 295	
tat gaa ggg gag gaa cat tgc ttc cag atc tac cat cct gaa act gag	964
Tyr Glu Gly Glu Glu His Cys Phe Gln Ile Tyr His Pro Glu Thr Glu	
300 305 310	
aat tct aaa gat ctc atc ggt cgc atc gct tcc ttc ctt gtt	1006
Asn Ser Lys Asp Leu Ile Gly Arg Ile Ala Ser Phe Leu Val	
315 320 325	
tgaacacaca gctagacttc gggttcatta ttactagtat gtgatttgt ttgattaatg	1066
ttttgtcatc aattgatggg taataaattg gattagggtt ctagggttcc tgaatcatgc	1126
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Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile	
35 40 45	
Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His	
50 55 60	
His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala	
65 70 75 80	
Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn	
85 90 95	
Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg	
100 105 110	
Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr	
115 120 125	
Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn	
130 135 140	
Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val	
145 150 155 160	

Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg
 165 170 175
 Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu
 180 185 190
 Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala
 195 200 205
 Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala
 210 215 220
 Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys
 225 230 235 240
 Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu
 245 250 255
 Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr
 260 265 270
 His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe
 275 280 285
 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
 290 295 300
 His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val
 305 310 315

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 <222> (1)..(957)

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 Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala
 20 25 30
 tcc cct gaa gat ccc caa act gga gtc tca tcc aaa gac ata gtc atc
 Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile
 35 40 45
 gca gac aac ccc tac gtc tcc gct cgc att ttc ctt ccc aaa tcc cac
 Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His
 50 55 60

cac act aac aac aaa ctc ccc atc ttc ctc tac ttc cac ggt ggc gcc	240
His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala	
65 70 75 80	
ttt tgc gtc gaa tcc gcc ttc tcc ttt ttc gtc cac cgc tat ctc aac	288
Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn	
85 90 95	
atc ttg gcc tca gaa gcc aac ata ata gcc atc tcc gtc gac ttc aga	336
Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg	
100 105 110	
ctc ctc cca cac cac cct atc cct gct gcc tac gaa gac ggt tgg acc	384
Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr	
115 120 125	
acc ctc aaa tgg att gct tcc cac gcc aac aac acc aac acc acc aac	432
Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Asn	
130 135 140	
ccg gag cca tgg cta ctc aac cac gcc gac ttc acc aaa gtc tac gta	480
Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val	
145 150 155 160	
gga ggt gaa acc agc ggt gct aac atc gca cac aac ctg ctt ttg cgt	528
Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg	
165 170 175	
gca ggt aac gaa tcc ctc ccc ggg gat ctg aaa ata ttg ggt gga tta	576
Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu	
180 185 190	
cta tgc tgc ccc ttc ttc tgg ggc tcg aag cca att ggg tcg gag gct	624
Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala	
195 200 205	
gtt gag ggg cac gag cag agt ttg gcc atg aag gtc tgg aac ttt gcc	672
Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala	
210 215 220	
tgc cct gat gcc ccc ggt gga atc gat aac ccc tgg atc aac ccc tgt	720
Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys	
225 230 235 240	
gtt cct ggg gca ccc tct ttg gcc act ctt gcc tgc tct aag ttg ctc	768
Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu	
245 250 255	
gtt act atc act ggc aaa gac gag ttc aga gac aga gat att ctc tac	816
Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr	
260 265 270	
cac cac acc gtt gag caa agt ggc tgg caa ggt gaa ctt caa ctc ttt	864
His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe	
275 280 285	

gat gct ggc gat gag gag cat gct ttc cag ctc ttc aag cct gag act 912
 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
 290 295 300

cat ctt gct aaa gcc atg atc aaa cgc ttg gct tct ttt ctg gtt tga 960
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<210> 5
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 <212> DNA
 <213> Artificial Sequence

<220>
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 primer

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<210> 6
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 6
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<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 7
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<210> 8
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic
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<210> 10
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